REMARKS

The Office Action of January 25, 2005 presents the examination of claims 83-124. These claims remain pending.

A minor housekeeping matter

Applicants' Representative has noted that the Examiner has not yet returned an initialed copy of the form PTO-1449 filed with the Information Disclosure Statement filed on May 17, 2004. The Examiner is requested to please consider the references listed therein (copy attached) and to return an initialed copy of the form PTO-1449 with the next Office communication.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 83, 84 and 86-124 are rejected under 35 U.S.C. § 112, second paragraph, as allegedly being indefinite. In particular, the Examiner indicates that the metes and bounds of the term "corresponding to" in these claims cannot be determined.

This rejection is respectfully traversed. Reconsideration and withdrawal thereof are requested.

> The requirement to "distinctly" claim means that the claim must have a meaning discernible to one of ordinary skill in the art when construed according to correct principles. *Union Pac. Res. Co. v. Chesapeake Energy Corp.*, 236 F.3d 684, 692 [57 USPQ2d 1293] (Fed. Cir. 2001); *Rosemount, Inc. v. Beckman Instruments, Inc.*, 727 F.2d 1540, 1547 [221 USPQ 1] (Fed. Cir. 1984). Only when a claim remains insolubly ambiguous without a discernible meaning after all reasonable attempts at construction must a court declare it indefinite. *Exxon Research & Eng'g Co. v. United States*, 265 F.3d 1371, 1375 [60 USPQ2d 1272] (Fed. Cir. 2001).

Metabolite Laboratories Inc. v. Laboratory Corp. of America Holdings, 71 USPQ2d 1081, 1089 (Fed. Cir. 2004).

> The second paragraph of §112 requires the specification of a patent to "conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention." 35 U.S.C. §112, ¶ 2 (2000). To satisfy this requirement, the claim, read in light of the specification, must apprise those skilled in the art of the scope of the claim. *See Miles Labs., Inc. v. Shandon, Inc.*, 997 F.2d 870, 875 [27 USPQ2d 1123] (Fed. Cir.

> 1993). Moreover, claims need not "be plain on their face in order to avoid condemnation for indefiniteness; rather, what [this court has] asked is that the claims be amenable to construction, however difficult that task may be." *Exxon Research & Eng'g Co. v. United States*, 265 F.3d 1371, 1375 [60 USPQ2d 1272] (Fed. Cir. 2001).
>
> *SmithKline Beecham Corp. v. Apotex Corp.*, 74 USPQ2d 1398, 1404 (Fed. Cir. 2005).

Applicants submit that the present claim language fully apprises one of ordinary skill in the art of molecular biology of the scope of claims 83, 84 and 86-124. These claims are fully amenable to construction and are not insolubly ambiguous.

The term "corresponding" or "corresponding to" is frequently used in the art of molecular biology to describe a relationship between two or more sequences identified by alignment of the sequences. Regions of substantial sequence identity define the alignment, and then the aligned sequence positions "correspond to" one another. The attached Exhibit 8, a small collection of abstracts taken from the Medline database, illustrate the common usage of this term.

Exhibit 8 amply demonstrates that a part of a nucleotide sequence "corresponding to" another sequence in the present claims is not at all indefinite, but rather identifies a part of a second sequence as aligned against a reference sequence. Accordingly, the instant rejection should be withdrawn.

Rejection under 35 U.S.C. § 112, first paragraph

Claims 83, 84 and 86-124 are rejected under 35 U.S.C. § 112, first paragraph, for alleged lack of adequate written description of the subject matter in the specification. This rejection is respectfully traversed. Reconsideration and withdrawal thereof are requested.

In particular, the Examiner asserts that the specification fails to describe those elements of a myosin light chain-2 promoter that are shared by the genus of such promoters. The Examiner argues that the term "corresponding to" admits of too much variation in scope and thus the specification does not describe concise structural features that define the genus.

Applicants strongly disagree. First, as explained above, the term "corresponding to" does not introduce so much variation as to abrogate any structural definition of the claimed sequence.

Second, the claims at issue expressly set forth elements of sequence that are found in a myosin light chain-2 promoter. For instance, claim 83 defines a fragment of from -19 to -800 nucleotides from the transcription start point in a mysosin light chain-2 promoter. The transcription start point is defined as a particular nucleotide in SEQ ID NO: 1, i.e. the one that corresponds to nucleotide 2406, in any such myosin light chain-2 promoter as may be aligned with SEQ ID NO: 1.

The particular features of a promoter that define it as a myosin light chain-2 promoter are expressly described in the second paragraph on page 15 of the English translation of the specification, and are also illustrated along the sequence of SEQ ID NO:1 in Figure 10. The attached Exhibit 9 is an alignment of the MLC-2 promoters from human, mouse and rat. The relevant elements as described in the specification are set forth in **bold** text. The Examiner will note that these elements are readily apparent as nearly completely conserved portions of the aligned sequences.

Applicants submit that the present specification very well describes structural elements that define the genus of a "myosin light chain-2 promoter". Description of the particular DNA elements that provide for the tissue-specific transcription properties of that promoter is provided in the specification and such evidences possession of the generic invention by the inventors at the time the application was filed. That is all that is required for adequate written description of an invention of generic scope. Accordingly, the instant rejection should be withdrawn.

Deposit requirement

The Examiner has maintained the rejection of claim 85 under 35 U.S.C. § 112, first paragraph for lack of enablement, requiring deposit of the vector expressly named in claim 85. Applicants are considering making the required deposit and, upon an indication from the Examiner that the other claims in the application are allowed, will either undertake the required deposit or cancel claim 85.

The present application well-describes and claims patentable subject matter. The favorable action of allowance of the pending claims and passage of the application to issue is respectfully requested.

Should there be any outstanding matters that need to be resolved in the present application, the Examiner is respectfully requested to contact Mark J. Nuell (Reg. No. 36,623) at the telephone number of the undersigned below, to conduct an interview in an effort to expedite prosecution in connection with the present application.

Dated: June 24, 2005

Respectfully submitted,

By _____

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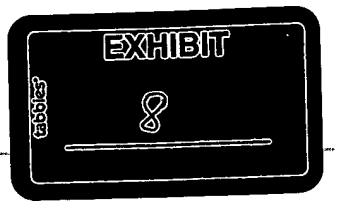
Attachments: Exhibits 8 and 9



5: Biochem Genet. 1996 Feb;34(1-2):31-43. Related Articles, Links

Molecular cloning of the mouse gene coding for carbonic anhydrase IV.

Tamai S, Cody LB, Sly WS.

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Carbonic anhydrase IV (CA IV) is expressed on apical surfaces of renal tubular epithelium and endothelium of specialized capillary beds. It plays a key role in bicarbonate reabsorption in kidney and in CO2 transport in other tissues. The human cDNA and genomic sequences have been cloned and characterized. Here we report the cloning and characterization of the entire mouse CA IV gene (contained in two overlapping lambda clones), which should enable generation of targeting constructs for disrupting the mouse CA IV gene to produce mouse models for in vivo analysis of CA IV gene function. The gene is approximately 8.2 kb long and contains eight exons ranging from 54 to 434 bp in length. The first exon (exon 1a) encodes the signal sequence. Exons 1b through 7 encode the remaining coding sequences. Exon 7 encodes the C terminus of the membrane-associated protein, as well as the 242-bp 3' untranslated sequence. The nucleotide sequence alignment between mouse and rat CA IV cDNAs reveals 84% identity. The nucleotide sequence alignment between mouse and human CA IV shows 69% identity in the coding region and all of the exon-intron boundaries are conserved, as are the sizes of the introns. The corresponding mouse and human exons are similar, except for the length of the untranslated regions in exons 1a and 7 and two small insertion/deletion events in exons 1a and 4. The 5' flanking region of the mouse gene (-300 to -1) is GC rich and contains 16 CpG dinucleotides. A TATA box sequence and several transcription factor binding sequences are identified upstream of exon 1a. Comparison of the nucleotide sequences surrounding the TATA box (-300 to -1) between mouse and human CA IV genes revealed 70% identity, indicating that regulatory sequences are as highly conserved as coding sequences between mouse and human CA IV genes.

PMID: 8935991 [PubMed - indexed for MEDLINE]

7: Gene. 1993 Dec 22;136(1-2):145-56.

Genomic sequences of murine gamma B- and gamma C-crystallin-encoding genes: promoter analysis and complete evolutionary pattern of mouse, rat and human gamma-crystallins.

Graw J, Liebstein A, Pietrowski D, Schmitt-John T, Werner T.

GSF-Institut fur Saugetiergenetik, Neuherberg, Germany.

The murine genes, gamma B-cry and gamma C-cry, encoding the gamma B- and gamma C-crystallins, were isolated from a genomic DNA library. The complete nucleotide (nt) sequences of both genes were determined from 661 and 711 bp, respectively, upstream from the first exon to the corresponding polyadenylation sites, comprising more than 2650 and 2890 bp, respectively. The new sequences were compared to the partial cDNA sequences available for the murine gamma B-cry and gamma C-cry, as well as to the corresponding genomic sequences from rat and man, at both the nt and predicted amino acid (aa) sequence levels. In the gamma B-cry promoter region, a canonical CCAAT-box, a TATA-box, putative NF-I and C/EBP sites were detected. An R-repeat is inserted 366 bp upstream from the transcription start point. In contrast, the gamma C-cry promoter does not contain a CCAAT-box, but some other putative binding sites for transcription factors (AP-2, UBP-1, LBP-1) were located by computer analysis. The promoter regions of all six gamma-cry from mouse, rat and human, except human psi gamma F-cry, were analyzed for common sequence elements. A complex sequence element of about 70-80 bp was found in the proximal promoter, which contains a gamma-cry-specific and almost invariant sequence (crygpel) of 14 nt, and ends with the also invariant TATA-box. Within the complex sequence element, a minimum of three further features specific for the gamma A-, gamma B- and gamma D/E/F-cry genes can be defined, at least two of which were recently shown to be functional. In addition to these four sequence elements, a subtype-specific structure of inverted repeats with different-sized spacers can be deduced from the multiple sequence alignment. A phylogenetic analysis based on the promoter region, as well as the complete exon 3 of all gamma-cry from mouse, rat and man, suggests separation of only five gamma-cry subtypes (gamma A-, gamma B-, gamma C-, gamma D- and gamma E/F-cry) prior to species separation.

PMID: 8293998 [PubMed - indexed for MEDLINE]

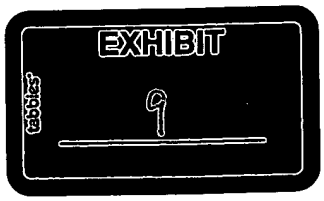
10: Gene. 1985;33(3):351-5.

Nucleotide sequence of a major class-III phage-T3 RNA-polymerase promoter located at 98.0% of phage-T3 genetic map.

Sarkar P, Sengupta D, Basu S, Maitra U.

The entire nucleotide sequence of a 409-bp HincII fragment, located within the MboI-E fragment on bacteriophage T3 DNA and containing a major class-III T3 RNA polymerase promoter positioned at 98% on the standard T3 genetic map, has been determined. Alignment of this class-III promoter with previously determined T3 RNA polymerase promoters, with start points of transcription (+1) in register, indicates high degree of sequence conservation between position -16 to +6 among all T3 RNA polymerase promoters. The conserved portion of the (-) strand sequence is 5'-A-TA-T-AT-A-C-C-C-T-C-A-C-T-A-A-A-G-G-G-A---3'. This fragment also contains an open reading frame (ORF) with a translational start codon located at position +146 which is preceded by a potential ribosome binding site (RBS). There is more than 70% amino acid-sequence homology between the deduced sequences of the -NH2 terminal region of this putative T3 phage protein and the corresponding protein coded by bacteriophage T7 (protein of T7 gene 19.5).

PMID: 2989096 [PubMed - indexed for MEDLINE]



CSS-ähnliche Sequenzen in den MLC-2v-Promotoren

CAGGG-ACACACACCCCCACTCGACTCTGGGGGCCCAGCC-CATCCTAAT human
CAGGG-ACAGAT-----CAC----CTCTGTGGGCCCAGACTCATAGTAAC Ratte
ATGGGGACA-----GGTTAC----CTCTGTGGGCCCAGGCTCACGGTAAA Maus

HF-3- und MLE1 Elemente in den MLC-2v-Promotoren

CTCTT **TAACCTTGAATGC** CTTTTTGGGGGC **TCACGTGTC-A** CCCAG human
CTCTT **TAACCTTGAAGGC** ATTTTTGGGT-C **TCACGTGTCCA** CCCAG Ratte
CTCTT **TAACCTTGAAGGC** ATTTTTGGGT-C **TCACGTGTCCA** CCCAG Maus
HF-3-Box MLE1-Box

HF-2-Element, E-Box, HF-1a- und HF-1b- Elemente in den MLC-2v-Promotoren

TGAGCCACC**CTTACTTCAGAAGAACGGC**ATGGGGTGGGGGGGCCTTAGGTGGTG human
TGAACGGCT**CTTACTTCAGAAGAACGGC**ATGGGGTGGGGGGGCTTAGGTGGCC Ratte
TGAGCAGCT**CTTACTTCAGAAGAACGGC**ATGGAGTGGGGGGTGGGGGGCTTAGG Maus
TGGCC HF-2-Box

CCCGCCTCACCTA **TGACTG** CCAAAA **GCGGTCATG** **GGGTTATTTTTA** human
TCTGCCTCACCTA **CAACTG** CCAAAA **GTGGTCATG** **GGGTTATTTTTA** Ratte
TCCGCCTCACCTA **CAACTG** CCAAAA **GTGGTCATG** **GGGTTATTTTTA** Maus
E-Box HF-1a-Box HF-1b-Box